

1642

RAW SEQUENCE LISTING      DATE: 05/31/2000  
 PATENT APPLICATION: US/09/250,056B      TIME: 13:26:44

Input Set : A:\ESPTO.txt  
 Output Set: N:\CRF3\05312000\I250056B.raw

5 <110> APPLICANT: Marks, James D  
 7      Poul, Marie A  
 11 <120> TITLE OF INVENTION: INTERNALIZING ERB2 ANTIBODIES  
 15 <130> FILE REFERENCE: 2500.116US3 Internalizing ErbB2 Ab  
 19 <140> CURRENT APPLICATION NUMBER: 09/250,056B  
 21 <141> CURRENT FILING DATE: 1999-02-12  
 25 <150> PRIOR APPLICATION NUMBER: 60/082,953  
 27 <151> PRIOR FILING DATE: 1998-04-24  
 31 <160> NUMBER OF SEQ ID NOS: 8  
 35 <170> SOFTWARE: PatentIn Ver. 2.0  
 39 <210> SEQ ID NO: 1  
 41 <211> LENGTH: 246  
 43 <212> TYPE: PRT  
 45 <213> ORGANISM: Artificial Sequence  
 49 <220> FEATURE:  
 51 <223> OTHER INFORMATION: Description of Artificial Sequence: scFv F5 amino  
 53      acid sequence  
 57 <220> FEATURE:  
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 61 <222> LOCATION: (31)..(35)  
 63 <223> OTHER INFORMATION: VH-CDR1  
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 69 <221> NAME/KEY: DOMAIN  
 71 <222> LOCATION: (50)..(66)  
 73 <223> OTHER INFORMATION: VH-CDR2  
 77 <220> FEATURE:  
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 81 <222> LOCATION: (99)..(108)  
 83 <223> OTHER INFORMATION: VH-CDR3  
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 91 <222> LOCATION: (157)..(170)  
 93 <223> OTHER INFORMATION: VL-CDR1  
 97 <220> FEATURE:  
 99 <221> NAME/KEY: DOMAIN  
 101 <222> LOCATION: (186)..(192)  
 103 <223> OTHER INFORMATION: VL-CDR2  
 107 <220> FEATURE:  
 109 <221> NAME/KEY: DOMAIN  
 111 <222> LOCATION: (225)..(235)  
 113 <223> OTHER INFORMATION: VL-CDR3  
 117 <400> SEQUENCE: 1  
 119 Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 121      1                      5                      10                      15  
 125 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Ser Tyr  
 127                      20                      25                      30  
 131 Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

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TC 1000 MAIL ROOM

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133          35          40          45
137 Ser Ala Ile Ser Gly Arg Gly Asp Asn Thr Tyr Tyr Ala Asp Ser Val
139          50          55          60
143 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
145          65          70          75          80
149 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
151          85          90          95
155 Ala Lys Met Thr Ser Asn Ala Phe Ala Phe Asp Tyr Trp Gly Gln Gly
157          100          105          110
161 Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
163          115          120          125
167 Ser Gly Gly Gly Gly Ser Gln Ser Val Leu Thr Gln Pro Pro Ser Val
169          130          135          140
173 Ser Gly Ala Pro Gly Gln Arg Val Thr Ile Ser Cys Thr Gly Ser Ser
175          145          150          155          160
179 Ser Asn Ile Gly Ala Gly Tyr Gly Val His Trp Tyr Gln Gln Leu Pro
181          165          170          175
185 Gly Thr Ala Pro Lys Leu Leu Ile Tyr Gly Asn Thr Asn Arg Pro Ser
187          180          185          190
191 Gly Val Pro Asp Arg Phe Ser Gly Phe Lys Ser Gly Thr Ser Ala Ser
193          195          200          205
197 Leu Ala Ile Thr Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys
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203 Gln Phe Tyr Asp Ser Ser Leu Ser Gly Trp Val Phe Gly Gly Gly Thr
205          225          230          235          240
209 Lys Leu Thr Val Leu Gly
211          245
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219 <211> LENGTH: 242
221 <212> TYPE: PRT
223 <213> ORGANISM: Artificial Sequence
227 <220> FEATURE:
229 <223> OTHER INFORMATION: Description of Artificial Sequence: scFv C1 amino
231      acid sequence
235 <220> FEATURE:
237 <221> NAME/KEY: DOMAIN
239 <222> LOCATION: (31)..(35)
241 <223> OTHER INFORMATION: VH-CDR1
245 <220> FEATURE:
247 <221> NAME/KEY: DOMAIN
249 <222> LOCATION: (50)..(66)
251 <223> OTHER INFORMATION: VH-CDR2
255 <220> FEATURE:
257 <221> NAME/KEY: DOMAIN
259 <222> LOCATION: (99)..(108)
261 <223> OTHER INFORMATION: VH-CDR3
265 <220> FEATURE:
267 <221> NAME/KEY: DOMAIN
269 <222> LOCATION: (157)..(167)

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 TC 1600 MAIL ROOM

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271 <223> OTHER INFORMATION: VL-CDR1
275 <220> FEATURE:
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279 <222> LOCATION: (184)..(190)
281 <223> OTHER INFORMATION: VL-CDR2
285 <220> FEATURE:
287 <221> NAME/KEY: DOMAIN
289 <222> LOCATION: (223)..(231)
291 <223> OTHER INFORMATION: VL-CDR3
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303 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
305           20           25           30
309 Ala Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
311           35           40           45
315 Ser Ser Ile Ser Gly Ser Ser Arg Tyr Ile Tyr Tyr Ala Asp Ser Val
317   50           55           60
321 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
323   65           70           75           80
327 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
329           85           90           95
333 Ala Lys Met Asp Ala Ser Gly Ser Tyr Phe Asn Phe Trp Gly Gln Gly
335           100          105          110
339 Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Gly
341           115          120          125
345 Ser Gly Gly Gly Gly Ser Glu Thr Thr Leu Thr Gln Ser Pro Ser Phe
347   130          135          140
351 Leu Ser Ala Phe Val Gly Asp Arg Ile Thr Ile Thr Cys Arg Ala Ser
353 145           150          155          160
357 Pro Gly Ile Arg Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys
359           165          170          175
363 Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val
365           180          185          190
369 Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
371   195          200          205
375 Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
377   210          215          220
381 Tyr Asn Ser Tyr Pro Leu Ser Phe Gly Gly Gly Thr Lys Val Glu Ile
383 225           230           235           240
387 Lys Arg
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397 <211> LENGTH: 738
399 <212> TYPE: DNA
401 <213> ORGANISM: Artificial Sequence
405 <220> FEATURE:
407 <223> OTHER INFORMATION: Description of Artificial Sequence: nucleic acid
409     encoding scFv F5 Ab
413 <400> SEQUENCE: 3

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415 cagggtgcagc tgggtggagtc tggggggaggc ttggtacagc ctgggggggtc cctgagactc 60
417 tcctgtgcag cctctggatt caccctttcgc agctatgccca tgagctgggt ccgccaggct 120
419 ccagggaagg ggctggagtg ggtctcagct attagtggtc gtggtgataa cacatactac 180
421 gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cagcgtgtat 240
423 ctgcaaatga acagcctgag agccgaggac acggccggtt attactgtgc gaaaatgaca 300
425 agtaacgcgt tcgcatttga ctactggggc cagggaaccc tggtcaccgt ctctcaggt 360
427 ggaggcggtt caggcggagg tggctctggc ggtggcggat cgcagtctgt gttgacgcag 420
429 ccgccctcag tgtctggggc ccagggcag agggtcacca tctctgcac tgggagcagc 480
431 tccaacatcg gggcagggtta tgggtgtcac tgggtaccag agcttcacag aacagcccc 540
433 aaactcctca tctatggtaa caccaatcgg ccctcagggg tccctgaccg attctctggc 600
435 ttcaagtctg gcacctcagc ctccctggcc atcactgggc tccaggctga ggatgaggct 660
437 gattattact gccagttcta tgacagcagc ctgagtgggt ggggtgttcg cggaggggacc 720
439 aagctgaccg tgctaggt 738
443 <210> SEQ ID NO: 4
445 <211> LENGTH: 726
447 <212> TYPE: DNA
449 <213> ORGANISM: Artificial Sequence
453 <220> FEATURE:
455 <223> OTHER INFORMATION: Description of Artificial Sequence: Nucleic acid
457 encoding scFv C1 amino acid sequence
461 <220> FEATURE:
463 <221> NAME/KEY: modified_base
465 <222> LOCATION: (111)
467 <223> OTHER INFORMATION: N = A, C, G, OR T
471 <400> SEQUENCE: 4
473 cagggtgcagc tgggtggagtc tggggggaggc ttggtacagc ctgggggggtc cctgagactc 60
475 tcctgtgcag cctctggatt caccctttagc agctatgccca tgggctgggt ccgccaggct 120
477 ccagggaagg ggctggagtg ggtctcatca attagtggca gtatgata catatattac 180
479 gcagactccg tgaagggccg gttcaccatc tcccagagaca attccaagaa cagcgtgtat 240
481 ctgcaaatga acagcctgcg agccgaggac acggccggtt attactgtgc gaaaatggat 300
483 gcttcgggga gttatttttaa tttctggggc cagggcaccc tggtcaccgt ctctcaggt 360
485 ggaggcggtt caggcggagg tggctctggc ggtggcggat cggaaacgac actcacgcag 420
487 tctccatcct tctgtctgc attttagga gacagaatca ccatcactg ccgggccagt 480
489 ccgggcatta ggaattattt agcctggat cagcaaaaac cagggaagc ccctaagctc 540
491 ctgactctatg ctgcatctac tttgcaaagt ggggtcccat caagggtcag cggcagtgga 600
493 tctgggacag attttactct caccatcagc agcctgcagc ctgaagattt tgcaacttat 660
495 tattgtcaac aatataatag ttaccctctc agtttcggcg gagggaccaa ggtggagatc 720
497 aaacgt 726
501 <210> SEQ ID NO: 5
503 <211> LENGTH: 5
505 <212> TYPE: PRT
507 <213> ORGANISM: Artificial Sequence
511 <220> FEATURE:
513 <223> OTHER INFORMATION: Description of Artificial Sequence: translocation
515 sequence
519 <400> SEQUENCE: 5
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523 1 5
529 <210> SEQ ID NO: 6

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Input Set : A:\ESPTO.txt  
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531 <211> LENGTH: 4  
533 <212> TYPE: PRT  
535 <213> ORGANISM: Artificial Sequence  
539 <220> FEATURE:  
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551    1  
557 <210> SEQ ID NO: 7  
559 <211> LENGTH: 4  
561 <212> TYPE: PRT  
563 <213> ORGANISM: Artificial Sequence  
567 <220> FEATURE:  
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579    1  
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589 <212> TYPE: PRT  
591 <213> ORGANISM: Artificial Sequence  
595 <220> FEATURE:  
597 <223> OTHER INFORMATION: Description of Artificial Sequence:: translocation  
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605 Lys Asp Glu Leu  
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VERIFICATION SUMMARY

DATE: 05/31/2000

PATENT APPLICATION: US/09/250,056B

TIME: 13:26:45

Input Set : A:\ESPT0.txt

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